

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 06:10:02 ; Search time 293 Seconds  
(without alignments)  
5296.284 Million cell updates/sec

Title: US-10-612-379-1

Perfect score: 873

Sequence: 1 atggcagaagcttaccagat.....ccgatgtaattgtcattaa 873

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/6C\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/6D\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/6E\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/6F\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/6G\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76.4	8.8	1090	3	US-09-270-767-26167
2	76.4	8.8	1880	3	US-09-270-767-10712
3	47.4	5.4	7218	2	US-08-232-463-14
4	46.4	5.3	819	3	US-08-792-014-2
5	46.4	5.3	819	3	US-08-443-948-2
6	46.4	5.3	819	3	US-09-690-196-2
7	43.4	5.0	1652	3	US-09-620-312D-815
8	43.4	5.0	1689	3	US-09-949-016-5780
9	42.8	4.9	2335	3	US-10-104-047-1220
10	41	4.7	1068	3	US-09-710-794-3
11	39.8	4.6	601	3	US-09-949-016-107953
12	39.8	4.6	601	3	US-09-949-016-107954
13	39.8	4.6	390890	3	US-09-949-016-14720
14	39.2	4.5	1529	3	US-09-533-029-49
15	38.4	4.4	1141	3	US-09-806-708B-22
16	38.4	4.4	253345	3	US-09-949-016-12656
17	38.4	4.4	253364	3	US-09-949-016-13639
18	37.8	4.3	832	3	US-09-621-976-2813
19	37	4.2	14066	3	US-09-601-198-56
20	36.8	4.2	1664976	3	US-08-916-421B-1
21	36.8	4.2	1664976	3	US-09-692-570-1
22	36.2	4.1	50000	3	US-09-662-254B-23
23	36	4.1	42381	3	US-09-949-016-12012
24	36	4.1	168394	3	US-09-949-016-13002

25	36	4.1	183770	3	US-09-949-016-15494	Sequence 15494, A
26	35.8	4.1	95561	3	US-09-949-016-12768	Sequence 12768, A
27	35.8	4.1	95561	3	US-09-949-016-13306	Sequence 13306, A
28	35.8	4.1	95561	3	US-09-949-016-13307	Sequence 13307, A
C 29	35.6	4.1	601	3	US-09-949-016-86515	Sequence 86515, A
30	35.6	4.1	61462	3	US-09-949-016-17522	Sequence 17522, A
C 31	35.6	4.1	183112	3	US-09-949-016-14184	Sequence 14184, A
C 32	35.4	4.1	601	3	US-09-949-016-141596	Sequence 141596, A
C 33	35.4	4.1	832	3	US-09-621-976-2813	Sequence 2813, Ap
34	35.4	4.1	236964	3	US-09-949-016-15753	Sequence 15753, A
C 35	35.4	4.1	250715	3	US-09-949-016-13294	Sequence 13294, A
C 36	35	4.0	601	3	US-09-949-016-141597	Sequence 141597, A
37	35	4.0	1497	3	US-09-232-468A-17	Sequence 17, Appl
38	35	4.0	1497	3	US-09-784-984B-14	Sequence 14, Appl
39	34.6	4.0	696	3	US-09-583-110-1334	Sequence 1334, Ap
40	34.6	4.0	789	3	US-09-107-433-176	Sequence 176, App
41	34.6	4.0	921	3	US-09-270-767-8688	Sequence 8688, Ap
42	34.6	4.0	921	3	US-09-270-767-23970	Sequence 23970, A
43	34.2	3.9	1086	3	US-09-248-796A-59	Sequence 59, Appl
44	34.2	3.9	2082	3	US-09-248-796A-2564	Sequence 2564, Ap
C 45	34.2	3.9	343352	3	US-09-949-016-13498	Sequence 13498, A

#### ALIGNMENTS

##### RESULT 1

US-09-270-767-26167

; Sequence 26167, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 26167

; LENGTH: 1090

; TYPE: DNA

; ORGANISM: *Drosophila melanogaster*

US-09-270-767-26167

Query Match 8.8%; Score 76.4; DB 3; Length 1090;  
Best Local Similarity 52.5%; Pred. No. 7.2e-13;  
Matches 167; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

Qy	495	GCAACTATCCAAATATTCATCAGTTGCTATCCGAGAGAAATCTCGATATCTACTTGGAAA	554
Db	28	GCATCTCGCAAGATCAACGATCATCTGTCGCGCGCAACACGCGCTTCCTCACCGGCGA	87
Qy	555	CAGTATCAGTGNATATGACTGTGNACTGATGCCAGCTTTCATCATATTCGAATATTGG	614
Db	88	CACCATGTGCTGCTTCGACTGTGAGCTGATGCCGCGCTGCAGCACATCCGTGTGGCGG	147
Qy	615	ATTGTCACTTCTTGGATTTCGATATTCACATAATTTCACTCATCTCTGGGCTTATATCCT	674
Db	148	CAAGTACTTGTTCGACTTTGAATCCCGAGCACTTCACGCGCTTGGCGCTACATGTA	207
Qy	675	CAGTGCATACCGTACAGACATTTATAGAGTTGTCCGCGCGATCAGGACATATTATCA	734
Db	208	TCACATGTACAGCTGGAGCGCTTTCACAAATCGTGC CGCGCCGACGAGCATTTATCAA	267
Qy	735	TCATATAAGACAAATGATCTGTTCAAAATCAACGTTGAACCTTCCATCGCCAC	794
Db	268	TCACTACAGCTGCACAGAGTCTCAAAATGAAGACGAGAGCTGGAGAGCCGCCAC	327
Qy	795	AAAAACCCACACAATTTCC	812
Db	328	GTTTACCATACATATTC	345

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RESULT 2
US-09-270-767-10712
; Sequence 10712, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10712
; LENGTH: 1880
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10712

Query Match      8.8%; Score 76.4; DB 3; Length 1880;
Best Local Similarity 52.5%; Pred. No. 9.1e-13;
Matches 167; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 495 GCAACTATCCAAATATTGATCGTCTATCCGAGAGAAAATCTCGATATCTACTTGGAAA 554
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 818 GCATCTGGCAGATCAAGATCATCTGTCGCGCGCAACAGCGCTTCCTCACCGCGGA 877
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 555 CAGTATGACTGAATATGACTGTGAAGTATGATGCCAGTCTTTCATCATATTCGAATATTGG 614
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 878 CACCATGTGCTTCGACTGTGAGCTGATGCCGCGCTGCAGACACATCCGTGTGGCGGG 937
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 615 ATTGTCACCTTTGGAATTGATATTCACATATTTCACTATCTCTGGGCTTATATCT 674
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 938 CAACTACTTTGTCGACTTTTGAATCCCGACGCACTTGACGGCCCTGTGGCGCTACATGTA 997
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 675 CACTGCATACCGTCACAGCAGCATTTATTGAGAGTTGTCCCGCGATCAGGACATTATCA 734
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 998 TCACATGTACAGCTGGAGCGCTTCACACATCGTCGCGCGCGACAGGACATTATCA 1057
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 735 TCACATATAAGAACAAATGAATCTGTTCACAAATCAAGTGTAACCCCTCCAAATCCCAAC 794
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1058 TCACATACAGCTGCAACAGAGTCTCAAAATGAAGAAGCAGCAGGAGTGAGACGCCAC 1117
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 795 AAAAAGCGCACAAATCC 812
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1118 GTTACCATACATATTC 1135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
```



```
; APPLICATION NUMBER: 08/792,014
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0206 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-690-196-2

Query Match          5.3%; Score 46.4; DB 3; Length 819;
Best Local Similarity 50.0%; Pred. No. 0.00082;
Matches 116; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 540 ATATCTACTTGGAAACAGTATGACTGGAATATGACTGTGGAACCTGATGCCACGTCTTTCATCA 599
Db 546 ATTTCTGGATGCAATGAATGACATTAGCTGATTTGCAACCTGTGTCGCCCAAACTGCATAT 605
QY 600 TATTCGAATTATGATTTGTCTCTTGGATTTCGATATTCACATAATTTTCATCTCATCT 659
Db 606 TGTCAGGTGGTGGCCAAAATAATCGCAACTTTGATATTTCAAAGAAATGACTGGCAT 665
QY 660 CTGGGCTTATATCTCTCACTGTCATACCGTACAGCAGCATTTATTTGAGAGTTGTCCGCCGA 719
Db 666 CTGGAGATACCTTAACATATGATACAGTAGGACGGTTTCCACCAATACCTGTCCAGTGA 725
QY 720 TCAGGACATATTTATCATCATATATAAGAACAAATGAATCTGTTTCAAAATCAA 771
Db 726 TAAGGAGGTGGAATAGCATATAGTGTAGTACCAAAAGACTCAACCAAGTAA 777

RESULT 7
US-09-620-312D-815
; Sequence 815, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radofe T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
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; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 815
; LENGTH: 1652
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(975)
US-09-620-312D-815

Query Match          5.0%; Score 43.4; DB 3; Length 1652;
Best Local Similarity 52.5%; Pred. No. 0.009;
Matches 95; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 549 TGGAAACAGTATGACTGGAATATGACTGTGAACTGATGCCACGTCTTTCATCATATTCGAAT 608
Db 756 TGGGACCAGCTAACACTGGCTGATTGTAGCTTTTACCCAAGCTGAACATTTATTAAGT 815
QY 609 TATTGGATTGTCACCTCTTGGATTTCGATATTCACATAATTTCACTCATCTCTGGGCTTA 668
Db 816 TGCTGCCAAGAAATATCGTGACTTTGACATTTCCAGCAGAAATTTCCAGAGTCTGGCGTTA 875
QY 669 TATCCTCACTGCATACCGTACAGCAGCATTTATTGAGAGTTTGTCCCGCCGATCAGGACAT 728
Db 876 TCTCCACAATGCCTATGCCCGTGAAGAATTTTACCACACGTTCTCTGAAGACAAGAAAT 935
QY 729 T 729
Db 936 T 936

RESULT 8
US-09-949-016-5780
; Sequence 5780, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5780
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5780

Query Match          5.0%; Score 43.4; DB 3; Length 1689;
Best Local Similarity 52.5%; Pred. No. 0.0091;
Matches 95; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 549 TGGAAACAGTATGACTGGAATATGACTGTGAACTGATGCCACGTCTTTCATCATATTCGAAT 608
Db 746 TGGGACCAGCTAACACTGGCTGATTGTAGCTTTTACCCAAGCTGAACATTTATTAAGT 805
QY 609 TATTGGATTGTCACCTCTTGGATTTCGATATTCACATAATTTCACTCATCTCTGGGCTTA 668
Db 806 TGCTGCCAAGAAATATCGTGACTTTGACATTTCCAGCAGAAATTTCCAGAGTCTGGCGTTA 865
QY 669 TATCCTCACTGCATACCGTACAGCAGCATTTATTGAGAGTTTGTCCCGCCGATCAGGACAT 728
Db 866 TCTCCACAATGCCTATGCCCGTGAAGAATTTTACCACACGTTCTCTGAAGACAAGAAAT 925
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Qy	729	T	729
Db	926	T	926

## RESULT 9

```

US-10-104-047-1220
; Sequence 1220, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1220
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1220

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Query Match	4.9%;	Score 42.8;	DB 3;	Length 2335;
Best Local Similarity	50.5%;	Pred. No. 0.016;		
Matches 104;	Conservative 0;	Mismatches 102;	Indels 0;	Gaps 0;
QY	541	TATCTACTCGAAACAGTATGACTGGAATATGACTGTGAACGTGATGCCACGGTCTTCATCAT	600	
DB	375	TTTCTGGATGGGACGAGCTGACGCTGGCTGACTGCAACCTCTTACCCAGCTCCATATT	434	
QY	601	ATTTCGAATTATTGGATTGTCACTCTTTGGATTTCGATATTCCACATAATTTCACTCATCTC	660	
DB	435	ATTAAGAATTTGGGCCAGAAAGTACAGAGATTTTGAATTTCTCTCTGAAATGACTGGGCATC	494	
QY	661	TGGGCTTTATATCCTCACTGCATACCGTACAGCAGCATTTATTGAGAGTTGTCCCGCCGAT	720	
DB	495	TGAGATACTTTGAAATAATGCTTATGCTAGAGATGAGTTTCAAAATACGTGTCCAGCTGAT	554	
QY	721	CAGGACATTATTCACTATATAAGA	746	
DB	555	CAAGAGATTTGAACACGCATATTGAGA	580	

RESULT 10

```

RESOLD: 10
US-09-710-794-3
; Sequence 3, Application US/09710794
; Patent No. 6573069
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; TITLE OF INVENTION: NOVEL CRIB PROTEIN ZMSE1
; FILE REFERENCE: 99-76
; CURRENT APPLICATION NUMBER: US/09/710,794
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164,685
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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[illegible]

## RESULT 11

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US-09-949-016-107953
; Sequence 107953, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107953
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-107953

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Query Match	4.6%	Score 39.8;	DB 3;	Length 601;
Best Local Similarity	52.0%;	Pred. No. 0.072;		
Matches	89;	Conservative	0;	Mismatches 82; Indels 0; Gaps 0
Qy	324	TGTTCCACTCTTTGAAAAGGATCCATCCGCTGAGAAAGATACAGAACTTGTACAGAA	383	
Db	367	TGTAATACTCTGGAAAAAGTAACTTTAAGGAAGAAAGAACAGAAAGACAGTAACAGAAA	426	
Qy	384	CTTCAAACACTGTTCTCGCGACAAAAGTAGAGTTCGATAAGGGAAAAAGAGCCATCCAG	443	
Db	427	ATACTCTAGTTTCTGTGTAATAAGACTAATACCTAGGTATAAAATTCAGAGACGTCTCA	486	
Qy	444	AGTTGAAGATCTTCCACGACAGATTAAGTTCACTACAATCGAGCTGTGTGA	494	
Db	487	AGTTTAATAACTTCCAGTCCACATATATGATGTTTCCATTCTGTGCTTTGA	537	

## RESULT 12

US-09-949-016-107954  
; Sequence 107954, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107954
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-107954

Query Match          4.6%; Score 39.8; DB 3; Length 601;
Best Local Similarity 52.0%; Pred. No. 0.072;
Matches 89; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 324 TGTTCACACTTTTGAAGAGATCCATCCGCTGAGAGAGATAGAGAACTTGTACAGGAA 383
DB 368 TGTAAACACTCTGGGAAAAGTAACTTTAAGGAGAGAGAAAGACAGTAACAGAGAA 427

QY 384 CTTCAAACTGTTCCGCGAGCAAAAGTAGAGTTCCATAGGAGGAAAAGGAGCCATCGAG 443
DB 428 ATACTCTATGTTCCCTGTGTAATTAAGACTTAACCTAGGTAGTATTAATTCAGGACAGTCTCA 487

QY 444 AGTTGAAGATCTTCCAGCACAGATTAAGTTCACTACAACTCAGTCTGTGA 494
DB 488 AGTTTAATAACTTCCAGTCCACATATATGATGTTTCCATTCCTGCTGTGA 538

RESULT 13
US-09-949-016-14720/c
; Sequence 14720, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14720
; LENGTH: 390890
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(390890)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14720

Query Match          4.6%; Score 39.8; DB 3; Length 390890;
Best Local Similarity 52.0%; Pred. No. 1.2;
Matches 89; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
```

```
QY 384 CTTCAAACTGTTCCGCGAGCAAAAGTAGAGTTTCGATAGGGAAGGAGGACCATCGAG 443
DB 314175 ATACTCTATGTTCTGTGTAATAAAGACTAATACCTAGGTATATAAAATTCAGGACAGTCTCA 314116

QY 444 AGTTGAAGATCTTCCAGCACAGATTAAGTTTCACTACAACTCAGTCTGTGA 494
DB 314115 AGTTTAATAACTTCCAGTCCACATATATGATGTTTCCATTCCTGCTGTGA 314065

RESULT 14
US-09-533-029-49
; Sequence 49, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 1529
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G553
US-09-533-029-49

Query Match          4.5%; Score 39.2; DB 3; Length 1529;
Best Local Similarity 58.6%; Pred. No. 0.16;
Matches 68; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 150 TGAGATTGCGAGTTGCGACGAGTCGAGTCAAGACTGTCAACGTGAATTTCTGAAGCATTTAA 209
DB 249 TGAGTTGATGCTAGACCAGAGCATGATGAACAATAGAGTGAATTTACTTCTGTGA 308

QY 210 GAAGAACTTTCTCGGAGCACAAACCCAGTATATGATTGAAGAGGAAAAGAGCTGA 265
DB 309 TAATAACTCTCTTGAAGCAGAACCGTCGAGTAATAATGATCAGGACGAGACCGGA 364

RESULT 15
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
```

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/ TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match          4.4%; Score 38.4; DB 3; Length 1141;
Best Local Similarity 8.5%; Pred. No. 0.25;
Matches 36; Conservative 183; Mismatches 207; Indels 0; Gaps 0;

Qy 284 AGATTGAAGACCGATCTTTCATTTGGCAAGGAATTCAATGTTCCACTCTTTGAAAAGG 343
Db   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
176 DDDTKYHMNNNGCBTVMVRYKTRDWSBKRMNYGMBWKNWSYDVTTYWWDDMCK 235

Qy 344 ATCCATCCGCTGAGAAGAGAAATAGAGAACTTGTACAGGAACCTTCAAACCTGTTCTGCGAG 403
Db   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
236 RKVRVRVTRGRMRNYMVAFETAHRRRYNNGWTBAMAYRRWTMNNNNNAKAMCKRAKYW 295

Qy 404 CAAAGTAGAGTTCGATAAGGGAAGGAGCCATCGAGAGTTGAAGATCTTCCAGCAC 463
Db   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
296 GWRBVBVNSTCTTWKSKTKTKVTSWANNCRAGDANKDKWKWSAAMGVYNNNNNNNW 355

Qy 464 AGATTAAAGTTCACTACAATCGAGTCTGTGAGCAACTATCAATATTGATCAGTTGCTAT 523
Db   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
356 TYKARHBAWDWVHSAWKKWHAANAHAHYSRKKWTBYKRTMNNNNNGTTMWKEMAWYW 415

Qy 524 CCGAGAGAAATCTCGATATCTACTTGGAAACAGATGACTGAATATGACTGTGAAGTGA 583
Db   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
416 KMDMDWBGTYNNNNNGGRTYGYGWTKNKKMWTYYKWKANNCKWRADWDHKTCTHNNTTWKM 475

Qy 584 TGCCACGCTTTCATCATATTCGAATATTGGAATTGTCACCTTCTTGGATTGGATATCCAC 643
Db   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
476 KTYWNNCWKSMKNGKSHRBAAYVTWVWVRYAHNNNNNDYWWKACTWYKIBVCSK 535

Qy 644 ATAATTTCACTCATCTCTGGGCTTATATCTCTCACTGACATCCGACAGCAGCAATTATTG 703
Db   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
536 WNNYAAWYTKSSWNTSRYYRWKTNNSWRWRS DTRSGRANNYARABHYGYKWNTRWB 595

Qy 704 AGAGTT 709
Db   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
596 WSHTWB 601
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Search completed: March 15, 2006, 06:20:59  
Job time : 298 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2006, 20:15:22 ; Search time 23 Seconds  
(without alignments)  
1042.432 Million cell updates/sec

Title: US-10-612-379-7

Perfect score: 1515

Sequence: 1 MAEAYQIQSNGDPOSKPFLLE.....PEKVLDIRVKGLAPDVNVH 290

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	30.2	268	2	US-09-270-767-42304
2	272	18.0	120	2	US-09-270-767-57588
3	205.5	13.6	253	2	US-08-792-014-1
4	205.5	13.6	253	2	US-09-443-948-1
5	205.5	13.6	253	2	US-09-690-196-1
6	203.5	13.4	254	2	US-09-949-016-11651
7	198.5	13.1	241	2	US-09-387-372-3
8	198.5	13.1	241	2	US-09-949-016-11014
9	186	12.3	437	1	US-08-781-560-1
10	186	12.3	437	1	US-08-781-560-3
11	186	12.3	437	2	US-08-792-014-3
12	186	12.3	437	2	US-09-443-948-3
13	186	12.3	437	2	US-09-690-196-3
14	171	11.3	175	2	US-10-104-047-3190
15	158	10.4	210	1	US-08-781-560-4
16	158	10.4	210	1	US-08-933-750C-6
17	158	10.4	210	2	US-08-792-014-4
18	158	10.4	210	2	US-09-234-613-6
19	158	10.4	210	2	US-09-443-948-4
20	158	10.4	210	2	US-09-690-196-4
21	117	7.7	214	2	US-10-161-195-5
22	112	7.4	300	2	US-09-248-335-36
23	106.5	7.0	1261	2	US-09-949-016-9651
24	104	6.9	266	2	US-10-161-195-15
25	98.5	6.5	213	2	US-10-161-195-13
26	96	6.3	212	2	US-10-161-195-3
27	95	6.3	278	2	US-08-256-847C-5

28	94.5	6.2	212	2	US-10-161-195-7	Sequence 7, Appli
29	94.5	6.2	843	1	US-08-867-129-2	Sequence 2, Appli
30	94	6.2	432	2	US-09-389-681-181	Sequence 181, App
31	94	6.2	432	2	US-09-620-405B-181	Sequence 181, App
32	94	6.2	432	2	US-09-339-338-181	Sequence 181, App
33	94	6.2	432	2	US-09-433-826B-181	Sequence 181, App
34	94	6.2	432	2	US-09-604-287A-181	Sequence 181, App
35	94	6.2	432	2	US-09-285-480-181	Sequence 181, App
36	94	6.2	432	2	US-09-834-759-181	Sequence 181, App
37	94	6.2	432	2	US-09-590-751A-181	Sequence 181, App
38	94	6.2	432	2	US-09-551-621-181	Sequence 181, App
39	94	6.2	432	2	US-09-551-621A-181	Sequence 181, App
40	94	6.2	432	2	US-10-076-622-181	Sequence 181, App
41	94	6.2	1002	2	US-09-620-405B-475	Sequence 475, App
42	94	6.2	1002	2	US-09-604-287A-475	Sequence 475, App
43	94	6.2	1002	2	US-09-834-759-475	Sequence 475, App
44	94	6.2	1002	2	US-09-590-751A-475	Sequence 475, App
45	94	6.2	1002	2	US-09-551-621-475	Sequence 475, App

## ALIGNMENTS

### RESULT 1

US-09-270-767-42304  
; Sequence 42304, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42304  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-42304

Query Match 30.2%; Score 458; DB 2; Length 268;  
Best Local Similarity 40.4%; Pred. No. 4e-40;  
Matches 112; Conservative 42; Mismatches 89; Indels 34; Gaps 9;

Qy	3	EAYQIQ-SNGDPO-SKPLLELYKASGIDARRIGADLFCQEFWMELVALYIGVARVEVK	60
Db	13	ESQSQETNGSSKFDVDFEILIIKASTIDGRRKACLCQEFYFMDLYLLAEKTIISLKV	72
Qy	61	TANNVSEA--FKQNFLGAQPPIMIEBEKELTYTDNREIEGRIFHLAKEFNVP----	114
Db	73	TVDQKPPDPFRTNFEATHPPILI--DNGLAILENEKIER---HIMK--NIPGGVNLFPVQ	125
Qy	115	DPNAEKIENLYRNKFLFLRAKVEFDKCKEPEVEDLPAQIKVHYNRVCEQLSNIDOLL	174
Db	126	DKEVATLIENLYVKLLMLL---VKDEAKN-----NALLSHLRKINDHL	166
Qy	175	SEKRSYLLGNSTVEYDCELMPRLHRIIGLSLLGDFIDPHNFTLWAYILTAVRTAFI	234
Db	167	SARNTRELTGDTWCCFDCELMPRLQHRVAGKVFDFEIPHTLTALRYMYHMTQDAFT	226
Qy	235	ESCPADQDIHHYKQMNFTNQRETQSPKTKHTIP	271
Db	227	QSCPADQDIINHYKQSLKMKXGHELETFTFTTYP	263

### RESULT 2

US-09-270-767-57588  
; Sequence 57588, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

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; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57588
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57588

Query Match      18.0%; Score 272; DB 2; Length 120;
Best Local Similarity 47.7%; Pred. No. 6.2e-21;
Matches 53; Conservative 19; Mismatches 39; Indels 0; Gaps 0;

Qy 161 NRVCQSLNIDQLLSERKSRVLLGNSMTPEYDCELMPLRHRIIIGLSLLGDFDIPHNFTL 220
Db 5 NALLSLRKRINDLSARNTRELTGDMCCFCELMPLRLOHVRVAGKYFVDFEIPHTLAL 64

Qy 221 WAYILTAYRTAFTSCPADQDIHHYKEQWNLFTNORETLOSPTKTHTP 271
Db 65 WRYMYHQLDAFTQSCPADQDIHHYKLOQSLKMKKHEELETPTFTTYP 115

RESULT 3
US-08-792-014-1
; Sequence 1, Application US/08792014
; Patent No. 6063594
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN ANION CHANNEL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,014
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0206 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
US-08-792-014-1

Query Match      13.6%; Score 205.5; DB 2; Length 253;
Best Local Similarity 24.7%; Pred. No. 2.2e-13;

; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57588
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57588

Query Match      18.0%; Score 272; DB 2; Length 120;
Best Local Similarity 47.7%; Pred. No. 6.2e-21;
Matches 53; Conservative 19; Mismatches 39; Indels 0; Gaps 0;

Qy 161 NRVCQSLNIDQLLSERKSRVLLGNSMTPEYDCELMPLRHRIIIGLSLLGDFDIPHNFTL 220
Db 5 NALLSLRKRINDLSARNTRELTGDMCCFCELMPLRLOHVRVAGKYFVDFEIPHTLAL 64

Qy 221 WAYILTAYRTAFTSCPADQDIHHYKEQWNLFTNORETLOSPTKTHTP 271
Db 65 WRYMYHQLDAFTQSCPADQDIHHYKLOQSLKMKKHEELETPTFTTYP 115

RESULT 4
US-09-443-948-1
; Sequence 1, Application US/09443948
; Patent No. 6228616
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN ANION CHANNEL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/443,948
; FILING DATE: 19-NO. 6228616-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/792,014
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0206 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
US-09-443-948-1

Query Match      13.6%; Score 205.5; DB 2; Length 253;
Best Local Similarity 24.7%; Pred. No. 2.2e-13;

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RESULT 7
US-09-387-372-3
; Sequence 3, Application US/09387372A
; Patent No. 6461822
; GENERAL INFORMATION:
; APPLICANT: Gabel, Christopher A.
; APPLICANT: Griffiths, Richard J.
; APPLICANT: Egger, James F.
; APPLICANT: Campos, Manuel
; APPLICANT: Dombroski, Mark A
; APPLICANT: Geohagan, Kieran
; TITLE OF INVENTION: DIARYL SULFONYLUREA BINDING PROTEINS
; FILE REFERENCE: PC9860
; CURRENT APPLICATION NUMBER: US/09/387.372A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-387-372-3

Query Match      13.1%; Score 198.5; DB 2; Length 241;
Best Local Similarity 26.9%; Pred. No. 1.1e-12;
Matches 68; Conservative 49; Mismatches 99; Indels 37; Gaps 11;

QY      14  QSKPLLELYVKASGIDARRIGADLFCQEFWMELVALYBIGVARVEKTVNV--NSEAFKK 71
DB      3  EEQPOVELFVKA-GSDGAKIGNCPFSQRLFWMLK---GVT-FNVTVDTKRTETVQK 57
QY      72  NFLGAQPPIMIEEEKELTYTDNREIEGRIFHLAKEFNVPLFEK-----DPSAEKRIENLYR 127
DB      58  LCPGGQLPFLYGTE--VHTDTNKIEE--FLEAVLCPPPYPKLAALNPESNTAGLDIFA 112
QY      128  NFKLFLR-----AKVEFDKKGKPSRVED-----LPAQIKVHNVRCVCEQLSNIDQLLSE 176
DB      113  KFSAYIKNSPALNDNLEKGLLKALKVLDNYLTSPLEEV-----DETSAEDEGVQS 164
QY      177  RKSRYLLGNSMTEYDCELMPRLHRIIGLSLLGFDIPHNFTLHWAYILTYRTAAFTES 236
DB      165  RK--FLDGNELTLADCNLLPKLHIVQVCKYRGFTIPEAFRGVHRYLSNAYAREEF 222
QY      237  CPADQDIHHYKE 249
DB      223  CPDDEIELAYEQ 235

RESULT 8
US-09-949-016-11014
; Sequence 11014, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11014
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11014

Query Match      12.3%; Score 186; DB 1; Length 437;
Best Local Similarity 26.0%; Pred. No. 6e-11;
Matches 68; Conservative 45; Mismatches 95; Indels 54; Gaps 14;

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Qy	65	NSEAFKQNFGLGAQPPIMIEEBKITY-----TDNREIEGRIFHIAKEFNVPLPEKPD--S	117
Db	249	NNLA-----PGTHPPF-----LTFNGDVKTVDNKIE-----BFLBETLTP--EKYPRLA	290
Qy	118	AEKRIEN-----LYRNFKLFUR-----AKVEFDKG--KKEPSRVED-----LPAQIKVHYN	161
Db	291	AKHRESNTAGIDIFVKFSAYIKNTKQOSNAALERGLTKALKDDYINTLPEIDA----	347
Qy	162	RVCEQLSNIDQLLSERKSYILLGNSMTYDCELMPRLHHIRIICLSLLGDPDIPHNFTHLW	221
Db	348	----DTRGDEKGSRRK--FLDGBELTLADCNLLPKLHVVKYVAKKRYNVDFFPAEMTGLW	401
Qy	222	AYILTAYRTAAFTIESCPADQDI	243
Db	402	RYLKNAYARDEFTNTCAADSEI	423

RESULT 12

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RESULT 13

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US-09-690-196-3
; Sequence 3, Application US/09690196
; Patent No. 6503733
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
;           Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN ANION CHANNEL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 1174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/690,196
; FILING DATE: 16-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/792,014
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0206 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 289404
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-690-196-3

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Query Match	12.3%	Score 186;	DB 2;	Length 437;	
Best Local Similarity	26.0%;	Pred. No. 6e-11;			
Matches	68;	Conservative 45;	Mismatches 95;	Indels 54;	Gaps 14;
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Db	190	EGNSASASPINLFVKA-GIDGESIGNCPFSQRLFMILWIKGVVFNVT	VLDLKRKPADL	248	



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